

Abstract

Which genes are strongly biased to the leading strand?

- Essential genes
- Operons
 - Stronger bias for highly expressed or ubiquitous operons

Why are genes selected to the leading strand?

- Genes on the leading strand experience head-on collisions between DNA and RNA polymerases
- Head-on collisions slow the fork
 - Slowing the fork doesn't explain why essential genes show the strongest bias
- Head-on collisions interrupt gene expression for longer
 - Explains the strand bias of essential genes & operons

If Operons Were Independent of Bias

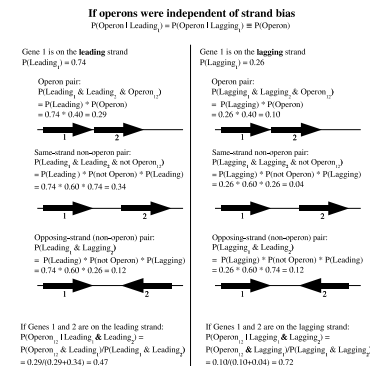
Operon pairs are

- closer together
- more conserved

Lagging-strand pairs are unlikely to arise unless they are operons (see right)

Lagging-strand pairs would be

- closer together
- more conserved



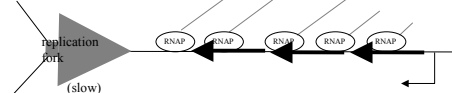
The Difference Between Strands

Operon on leading strand
Co-directional collisions



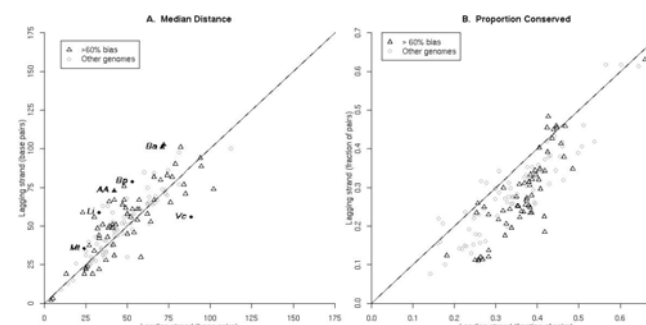
Interruptions:
1 s. for 1st gene
3 s. for 3rd gene

Operon on lagging strand
Head-on collisions



Interruptions:
5 s. for 1st gene
15 s. for 3rd gene

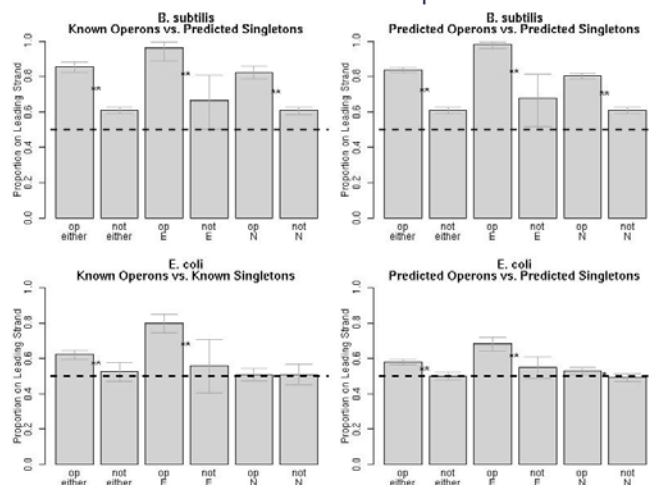
Operons Are Biased to the Leading Strand in Most Bacteria



Theories of Strand Bias

- Lagging strand slows the replication fork (Brewer)
 - Inconsistent with strong bias of essential genes relative to other highly expressed genes (Rocha)
- Toxic truncated peptide hypothesis (Rocha)
 - Does not explain bias of operons
 - Inconsistent with the peptide tag of tmRNA being non-essential
- Collisions (briefly) interrupt gene expression
 - Leading strand slows the fork => longer interruptions
 - Interrupting expression of essential genes or ubiquitous operons is more deleterious
 - Interruptions are longer for genes in operons
 - Interruptions are longer for highly expressed genes?
- Weak selective force => weak effect
 - Not observable for every chromosome or every type of gene

The Strand Bias of Operons



Stronger Bias for Highly Expressed and Ubiquitous Operons

